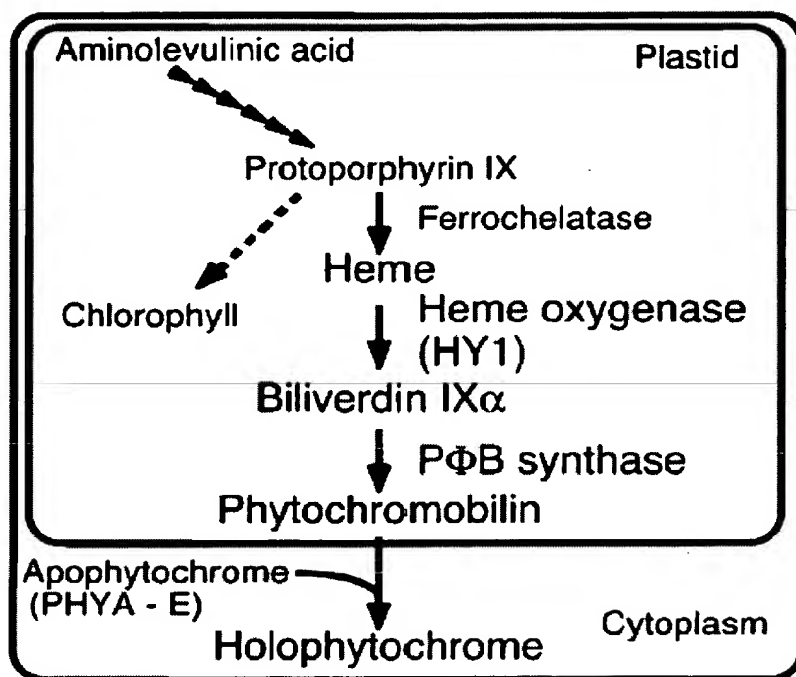
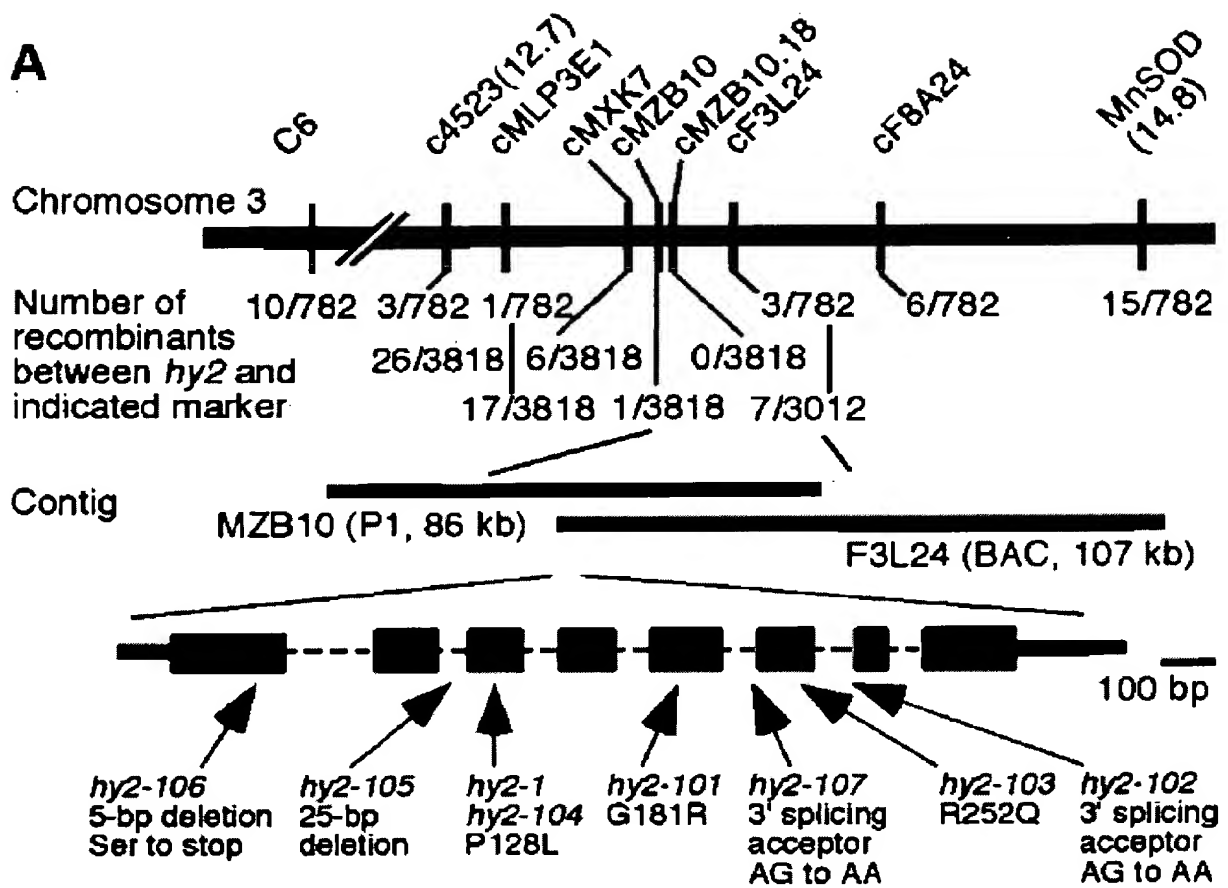


**Fig. 1**

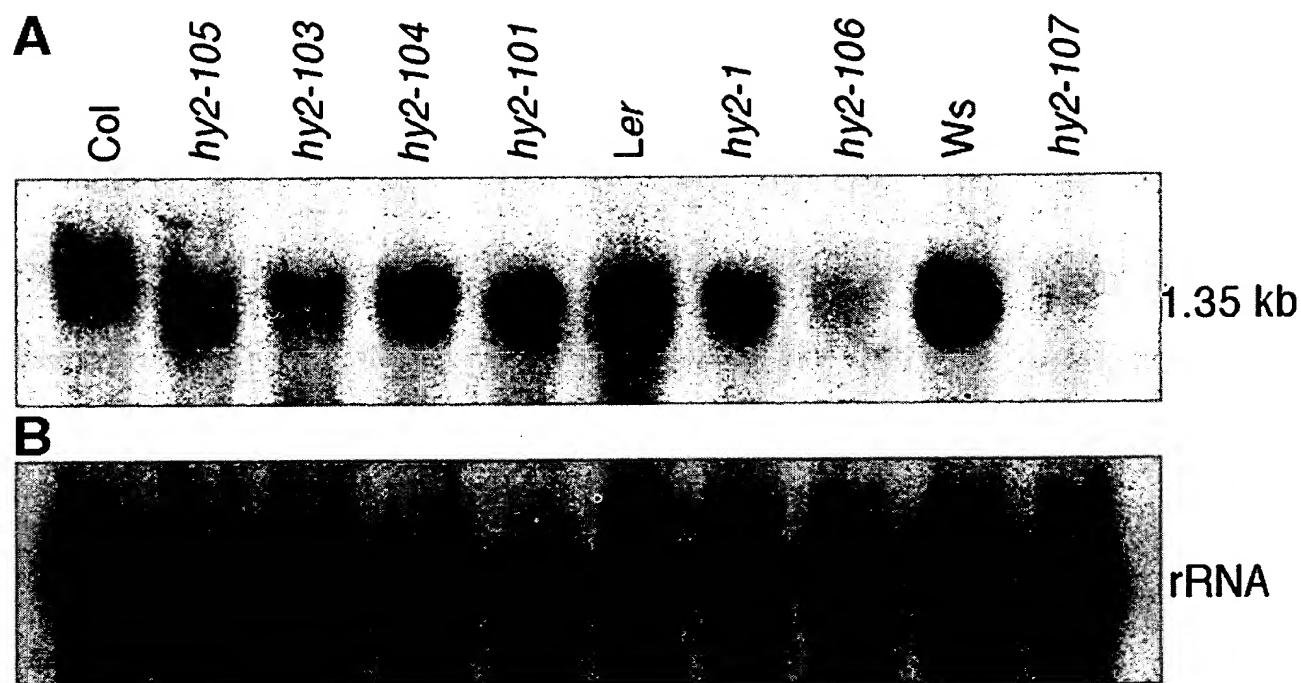


**Fig. 2**



**Fig. 3A**





**Fig. 4A and Fig. 4B**

```

      20      40      60      80
HY2_ARA1H : MALSHWFCFSIGSCPEAPKPEVLEBASFNKINFTLBRREK6FLRVERVEYKEFAESALEETRYRIVLESEHQEKYSSNICLDCR- : 86
YCP2_SYNPF : -----NFEHFWLKLKNDYTKR-----GSKGLSPKGLKKCRKKK- : 86
YHP2_FECMA : -----DKALMLQDLSEDLKKK1-18KCKM1KNGCKKKKVFHKQD- : 40
YHP2_FECMA : -----MIIRDYSLSKEDLRWINTPPFMDLVOKL-3VFEISVYSSCFLSKISITGSR : 54
YCP2_SYNPF : -----MTQRFSSTDPYMLIGWSTWPP7LEDALKEK-2GLEVESVTPDRFLQRIIDQIGSR : 54
SLR016 : -----MAVIDLELTN6SLMFTLWMIQQLALAEAA6M-QSLPLKGVQEPKGLCYVICRLECE : 56
      P 6

      100      120      140      160
HY2_ARA1H : -----TKLNTLTKKKKNTL-----SSMAFKK-KTLOVTFATENKRYVOTTFECANFTYTHVH--VVLGCHP-HQ1TDCRYQDKYV : 160
YCP2_SYNPF : -----GVGSDWMLDVVGVVDMVVDVLAQUSQVWVSGAYVYHEDVLCVVDLNVGAKOKLVAVLVSCVQVQ--DKVSLDVKYV : 116
YHP2_FECMA : -----CVTKSMMLDVVGVVDMVVDVLAQUSQVWVSGAYVYHEDVLCVVDLNVGAKOKLVAVLVSCVQVQ--DKVSLDVKYV : 116
YHP2_FECMA : RNPVNT777LWAAKFKNTDOVSLACGKGRSGVFFLHINDNDVOLFEGADYTFPHG--HILAKHSCPAKTL--DNTNTKTVSP : 137
YCP2_SYNPF : SKGIDVVDADWACKTERKPDQVLAACGACGASVLEFWINXGCGCLDFEGADYTFPHG--HILAKHSCPAKTL--DNTNTKTVSP : 137
SLR016 : -K---LVENRKYQIQPDKKHESLAKVCKGEMILHCUMFGRDLVCLDFEGADYTFPHG--HILAKHSCPAKTL--DNTNTKTVSP : 138
      d r g n p y f g l i t p

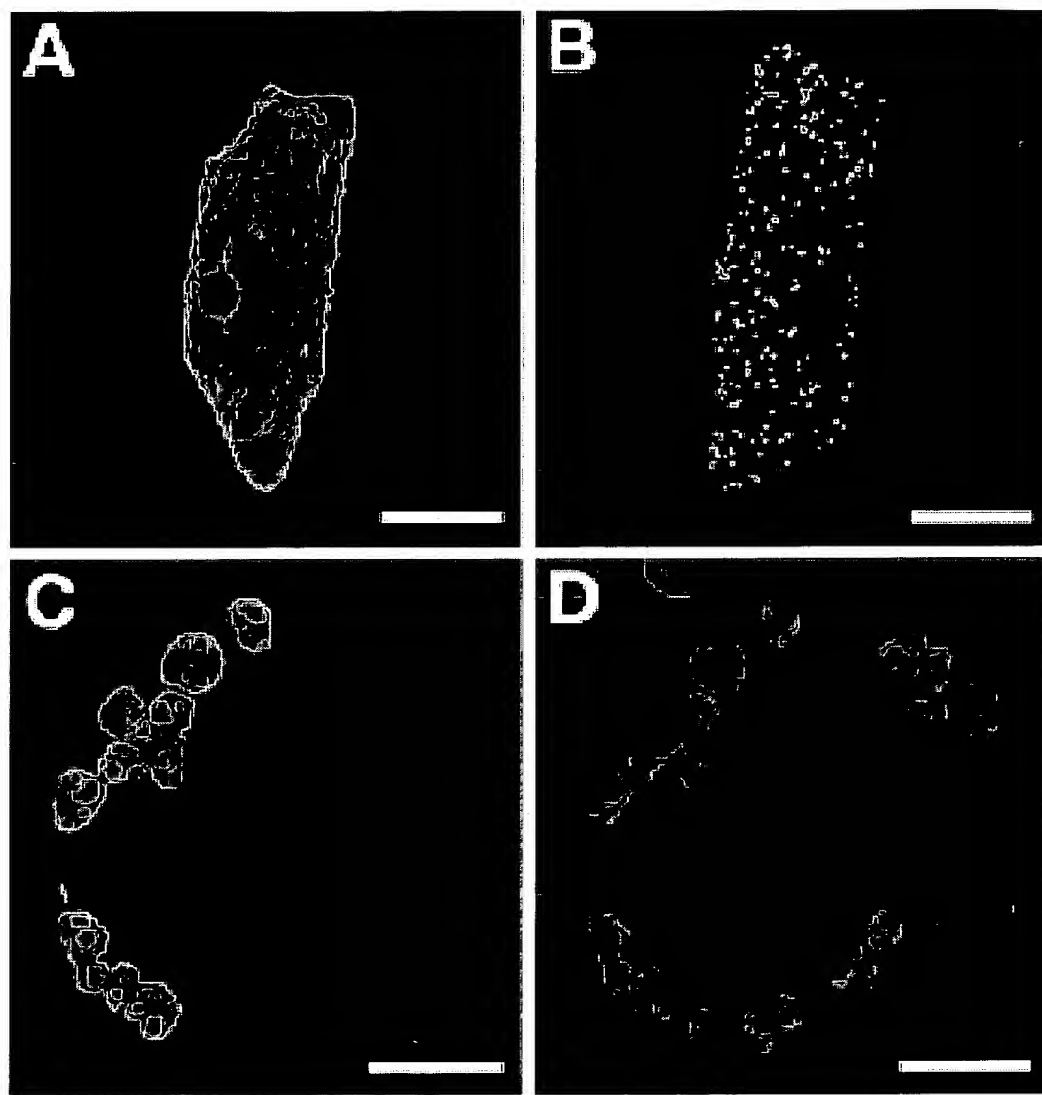
      180      200      220      240      260
HY2_ARA1H : KFM-----SYHFKTAKIFNWSKLGSIATFPLVMPTR-----FSSKKKKKKAIFSAFLSTYQALCEMTIQVREKMFPMVRANCBA : 244
YCP2_SYNPF : GPK-----SDNQRSFELNGESTMRSIDPNQVPSSTWLYCR-----GCAEQATLSLPEAFSAFYDANWDHNDNAKSPSCIPPEVEKHL : 193
YHP2_FECMA : CAG-----LKKKRSVDPSQKIMKIDDSNAPSPKVLTY-----GSPEDLQCSLAKILDSFHAHWQNDNMSREYIXIIFSKVEHL : 197
YHP2_FECMA : KLI-----VINDHQQLLPQGNIPKAKFVYVPGVMSVPLQKSTCHIISEIHPVAGGSEVLEIICLNIAKPLKAKK-ALKILSG : 219
YCP2_SYNPF : RPI-----PPEFELREGLRYGCPITPZACFEPFECFIFPBLPLGEGCELIQSINSPANWQNDLLELAAGAEKPTZER-SEVELSG : 219
SLR016 : SAEVGQPEFEGQRELEPPE-----ZTFKYLCKSLG-----FSKUTLEER77QGVVDLQTRCHQSTVREPLSLAQ-ILEHRS : 208
      E YK 6 r 51

      280      300      320      340
HY2_ARA1H : QHKLVLVRAQDYGCGGGLRLVYFAAKKELRDVLDGVDELQKTFVLDYVPEYVQVDDGTVDKRSIICKKSYKURFWOLFQDPIG : 329
YCP2_SYNPF : LKKKDISSAEKQFARGGPTSEFYADSSNRKHEFLSPASSSHK----- : 236
YHP2_FECMA : HIKKDISSAEKQFARGGPTSEFYADSSNRKHEFLSPASSSHK----- : 241
YHP2_FECMA : KKAIEKRSSTQDAAAMLCRSYFZETEDYHKKVEM----- : 257
YCP2_SYNPF : KKKCDLRABKQKARQMLTRESSETEAHTTVLQDL----- : 257
SLR016 : KIKKQQQKQKXTRMLKKNZFAAKKMSQVLDVTD----- : 248
      g y Dp E G V E L

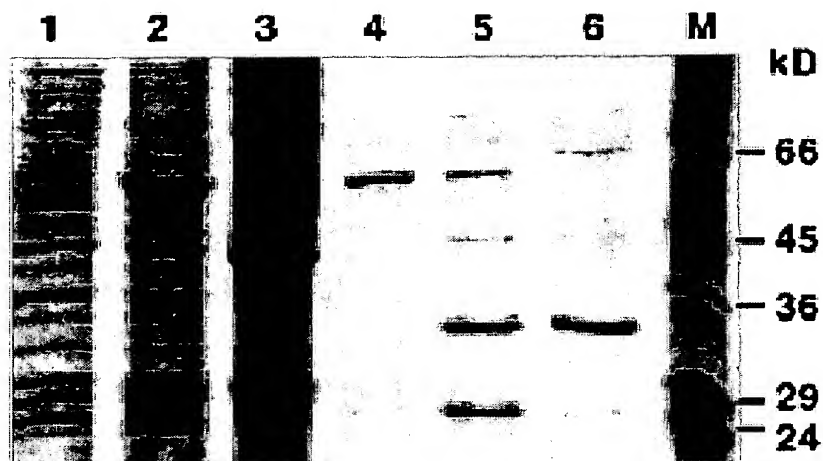
```

Fig. 5

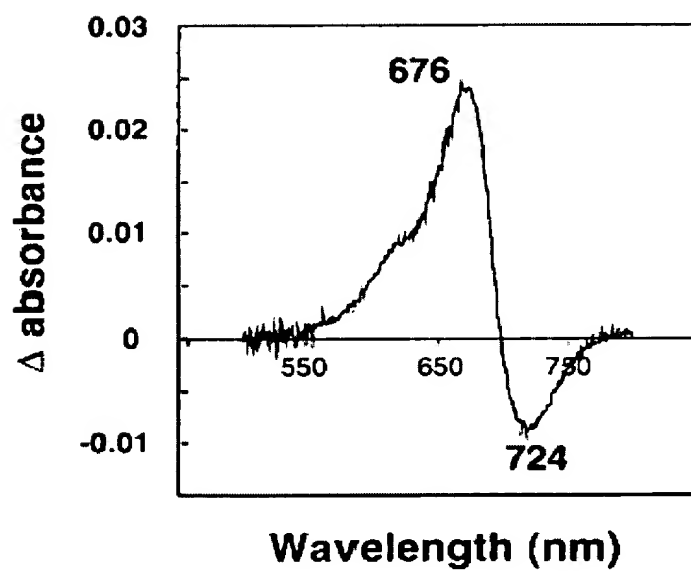
106250-90102860 0520405-052001



**Fig. 6A - 6D**

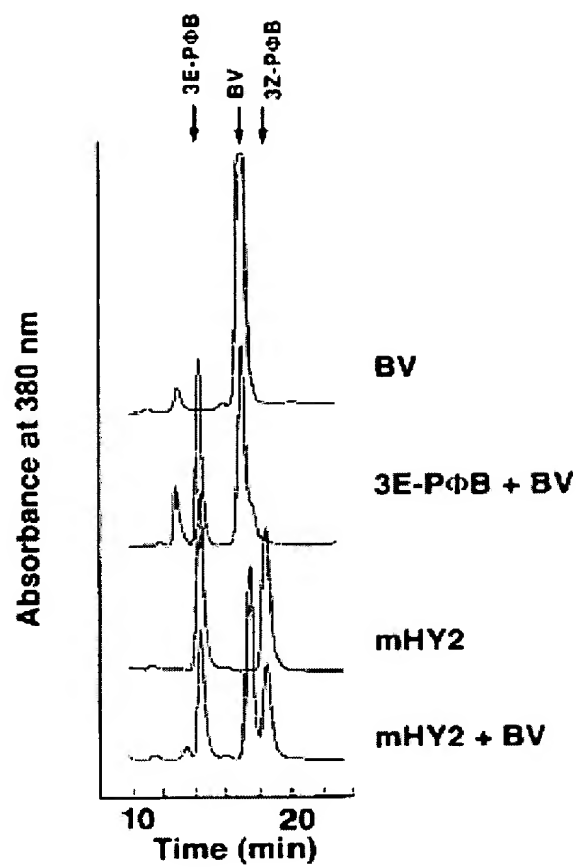


**Fig. 7**



**Fig. 8**





**Fig. 9**

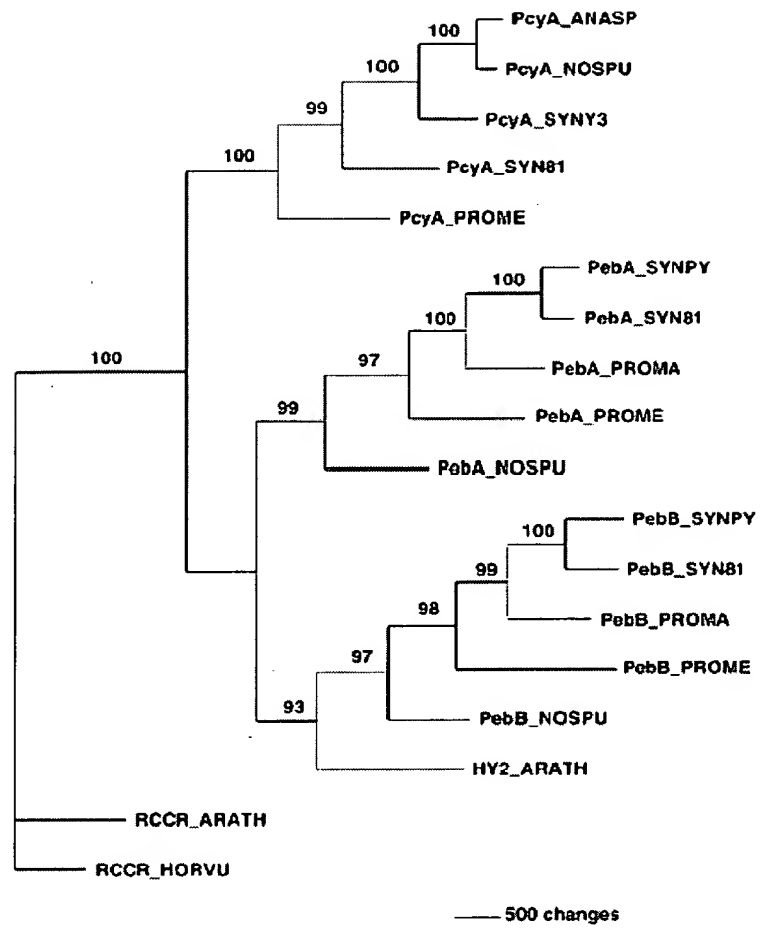
pcya_anasp	*	20	*	40	*	60	*	80	*	43
pcya_nospu	---	---	---	---	---	---	---	---	---	43
pcya_syny3	---	---	---	---	---	---	---	---	---	46
pcya_syn81	---	---	---	---	---	---	---	---	---	42
pcya_prome	---	---	---	---	---	---	---	---	---	44
peba_synpy	---	---	---	---	---	---	---	---	---	27
peba_syn81	---	---	---	---	---	---	---	---	---	27
peba_proma	---	---	---	---	---	---	---	---	---	31
peba_prome	---	---	---	---	---	---	---	---	---	25
peba_nospu	---	---	---	---	---	---	---	---	---	64
peba_synpy	---	---	---	---	---	---	---	---	---	44
pebb_syn81	---	---	---	---	---	---	---	---	---	45
pebb_proma	---	---	---	---	---	---	---	---	---	44
pebb_prome	---	---	---	---	---	---	---	---	---	37
pebb_nospu	---	---	---	---	---	---	---	---	---	40
hy2_arath	---	---	---	---	---	---	---	---	---	77
rccr_arath	---	---	---	---	---	---	---	---	---	90
rccr_horvu	---	---	---	---	---	---	---	---	---	4

pcya_anasp	*	100	*	120	*	140	*	160	*	180	
pcya_nospu	---	---	---	---	---	---	---	---	---	---	126
pcya_syny3	---	---	---	---	---	---	---	---	---	---	126
pcya_syn81	---	---	---	---	---	---	---	---	---	---	129
pcya_prome	---	---	---	---	---	---	---	---	---	---	123
peba_synpy	---	---	---	---	---	---	---	---	---	---	127
peba_syn81	---	---	---	---	---	---	---	---	---	---	109
peba_proma	---	---	---	---	---	---	---	---	---	---	109
peba_prome	---	---	---	---	---	---	---	---	---	---	113
peba_nospu	---	---	---	---	---	---	---	---	---	---	109
pebb_synpy	---	---	---	---	---	---	---	---	---	---	147
pebb_syn81	---	---	---	---	---	---	---	---	---	---	131
pebb_proma	---	---	---	---	---	---	---	---	---	---	132
pebb_prome	---	---	---	---	---	---	---	---	---	---	131
pebb_nospu	---	---	---	---	---	---	---	---	---	---	127
hy2_arath	---	---	---	---	---	---	---	---	---	---	124
rccr_arath	---	---	---	---	---	---	---	---	---	---	159
rccr_horvu	---	---	---	---	---	---	---	---	---	---	181

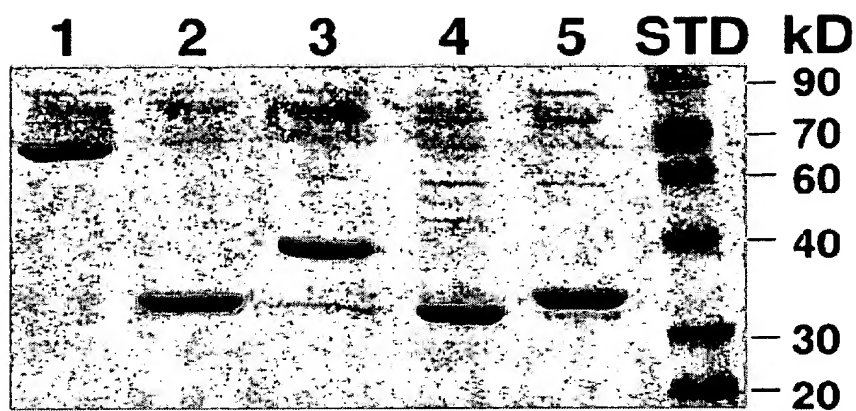
Fig. 10



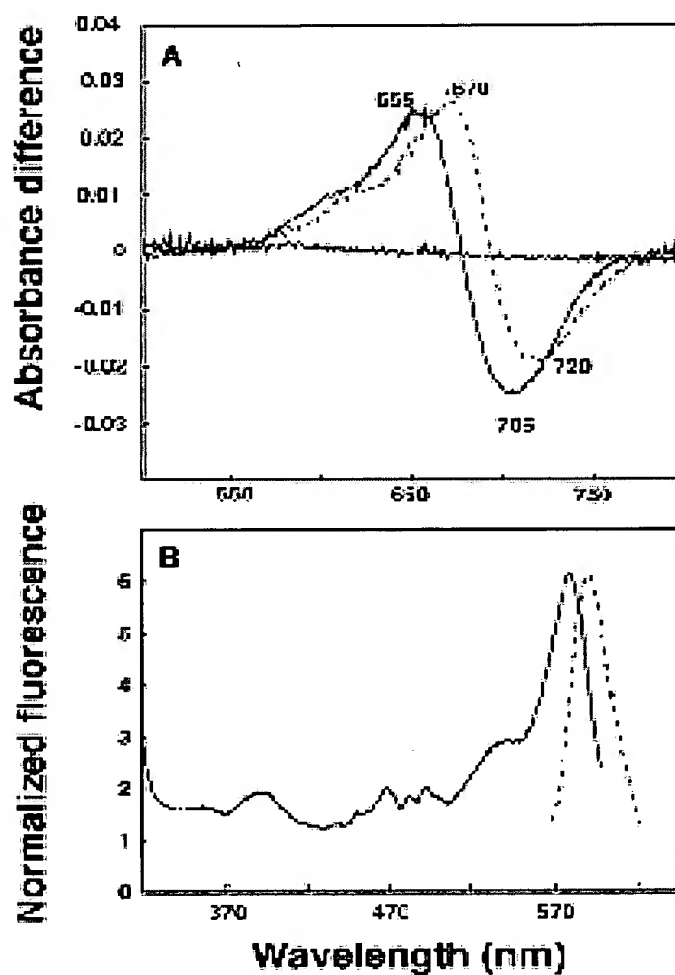
106250-9010250



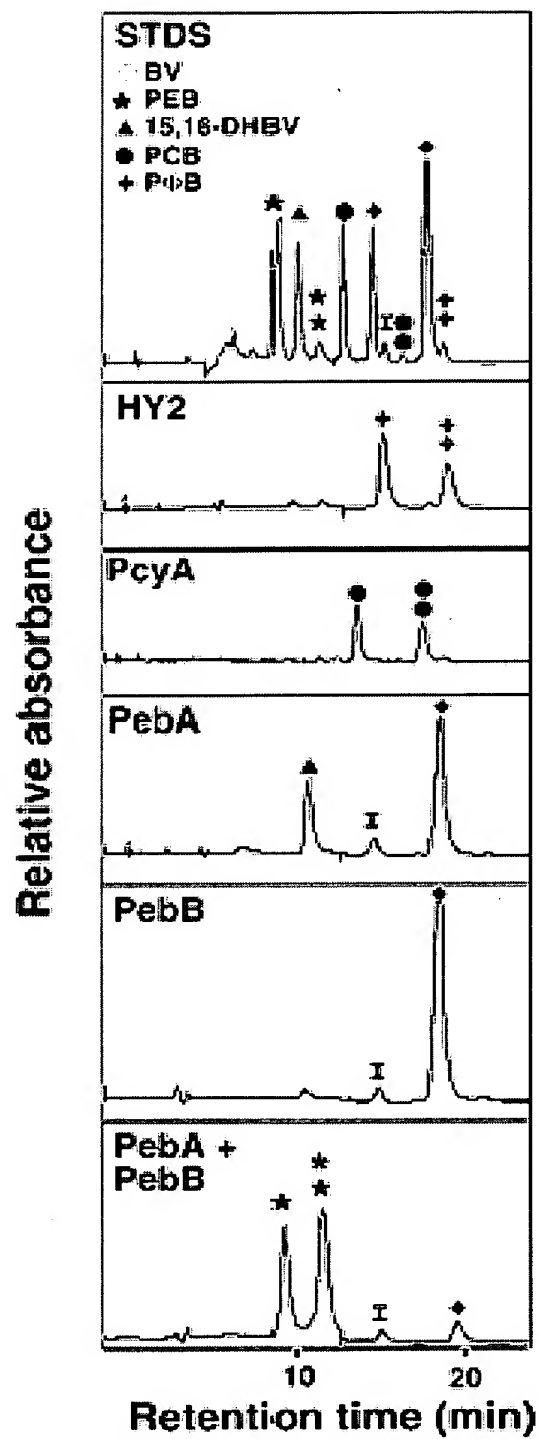
**Fig. 11**



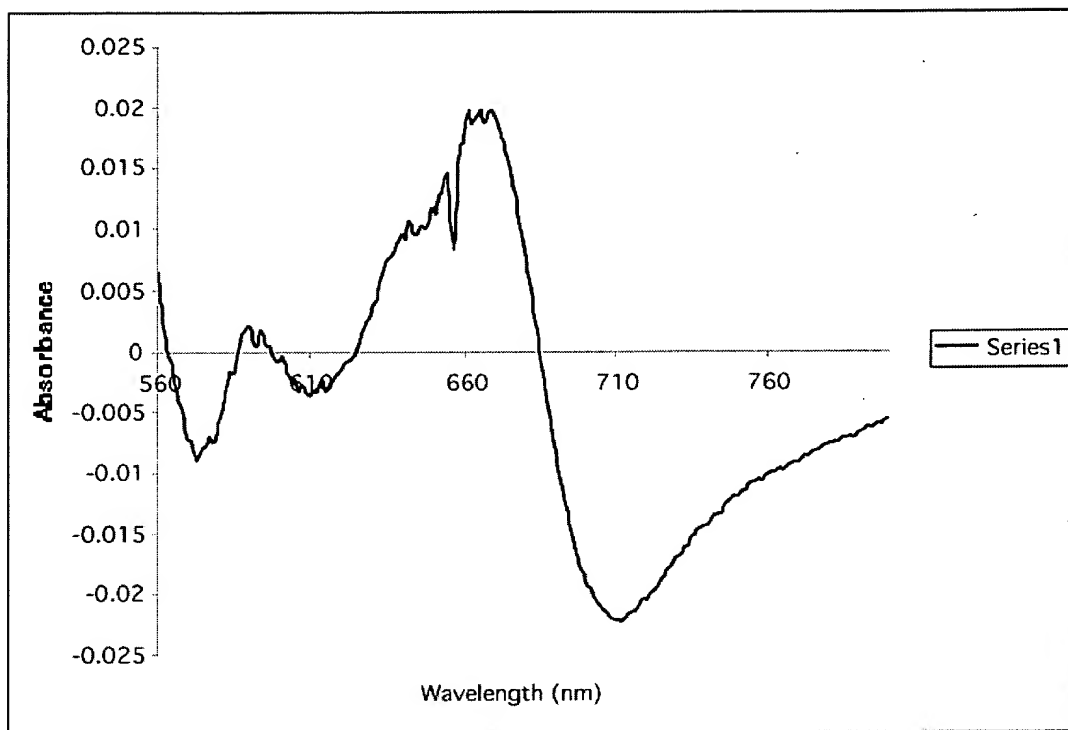
**Fig. 12**



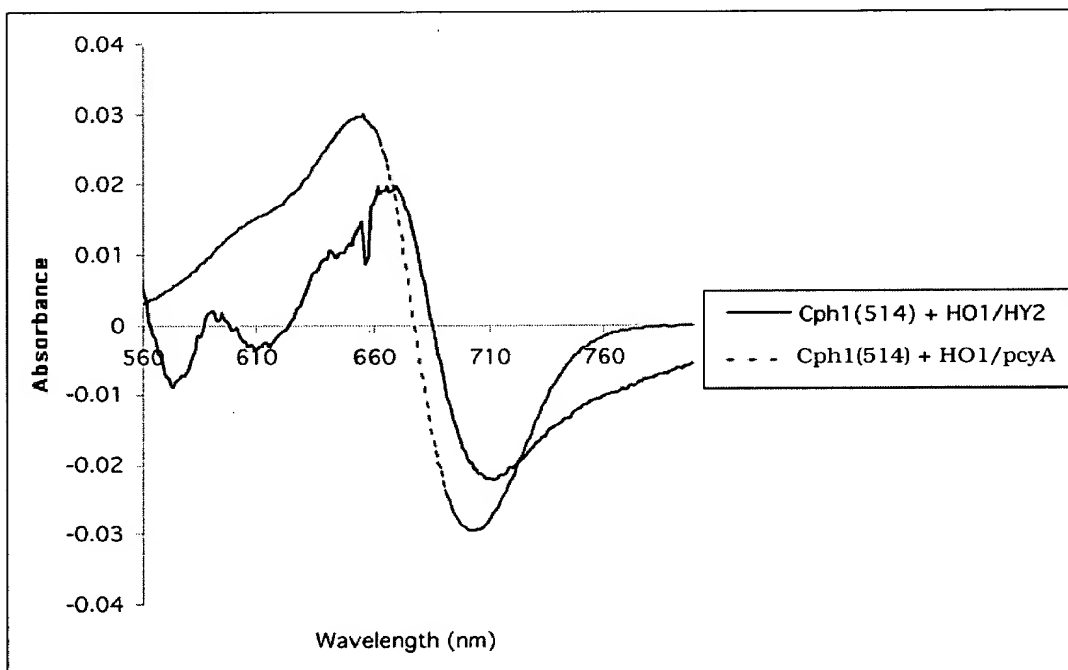
**Fig. 13A and 13B**



**Fig. 14**



**Fig. 15**



**Fig. 16**